

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:
 (A) NAME: Mitotix, Inc.
 (B) STREET: One Kendall Square, Building 600
 (C) CITY: Cambridge
 (D) STATE: MA
10 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 02139
 (G) TELEPHONE: (617) 225-0001
 (H) TELEFAX: (617) 225-0005

15 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
 Human Pathogens, and Uses Related Thereto

20 (iii) NUMBER OF SEQUENCES: 12

20 (iv) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: ASCII (text)

25 (vi) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/463,090
 (B) FILING DATE: 05-JUN-1995

30 (2) INFORMATION FOR SEQ ID NO:1:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 259..1491

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATGATACA AATGTGGAAG ATGCAAATTG TTCTTCCCCT ACTTGATGA GAAAAAGTGC	60
50 ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAAATAATT CCAAATCACC ATCGCCAATC	120
TTTTCAAATA CAAATGCAAC ATCTGGCTCT CCATTGTCAA ATCTTCTCG TGCACCATTG	180
AGAAATTAT CTAATTCGT TATTCTTCG TCAGTTAAAT CAAAAACGAA ACAATTAC	240
55 AACTCTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA Met Thr Glu Val Val Ser Lys Ser Ser His Ser	291

	TTT TTC AAT AAT TTG CAT CTT GCA ACC TCA ACT GCG TCT TCT TCA GTA Phe Phe Asn Asn Leu His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val	15	20	25	339
5	TCG AGC ACA ACT CCC AAA ATA GAA TTC AAT TCC ATA GCT GAA AAT GAT Ser Ser Thr Thr Pro Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp	30	35	40	387
10	GAT ATC CCT ACC AAT TAT GAC TCT GAT GAA GAA TTC GAA GAT GGT GAT Asp Ile Pro Thr Asn Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp	45	50	55	435
15	ACG TTT ATA CAA TCC ACC TTG ATT CAC CAG TTC AAC GCA AGT CAA GTA Thr Phe Ile Gln Ser Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val	60	65	70	483
20	ACA ACA ACA ACA ATA ATA ATA CCA ATG ATG GTA ACG ACA ATA ATA Thr Thr Thr Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile	80	85	90	531
25	TAC CTA CAA AAA TTA GAC GGT TCC ACT CCA TGT ACC AAA CCG ATA AAG Tyr Leu Gln Lys Leu Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys	95	100	105	579
30	AGA TTG CAT CGT ACC AAC TTC ATG AAG ATA ATT CAT TTT GAA ATT TAC Arg Leu His Arg Thr Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr	110	115	120	627
35	AAT ATT GAA TAT TCT CAT CTG GAG AGT GAT TTG TTA CCA CGA ATC GAT Asn Ile Glu Tyr Ser His Ser Glu Ser Asp Leu Leu Pro Arg Ile Asp	125	130	135	675
40	GCT CAT CAA TTA GCC AGA ATA TTA CGT GGA GAC CAC GAT GAC CAA TTT Ala His Gln Leu Ala Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe	140	145	150	723
45	GAT GAA TTT ATT ATC ATT GAT TGT CGA TTT GAG TAT GAA TTT AAT GGT Asp Glu Phe Ile Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly	160	165	170	771
50	GGC CAT ATT ACT AGG GCA ATC AAT ATC TCC ACC CAG GAA GCA CTT CAA Gly His Ile Thr Arg Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln	175	180	185	819
55	GAA AAG CTC TTT CAA TAT CAA GAA ACA GAT ACC AAG GAC ACT GAA AGC Glu Lys Leu Phe Gln Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser	190	195	200	867
60	AAG AAG CGA TTG ATA ATT TTC CAT TGT GAG TTC AGT ATG TTC AGA GGA Lys Lys Arg Leu Ile Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly	205	210	215	915
65	CCA ATG ATG GCC AAA CAT TTA AGA AAG TGT GAT AGA ATG TGC AAC TAC Pro Met Met Ala Lys His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr	220	225	230	963
70	GAC AAT TAT CCT CTA TTA ACA TAC CCC GAT ATT GCA ATT TTG GAA GGA Asp Asn Tyr Pro Leu Leu Thr Tyr Pro Asp Ile Ala Ile Leu Glu Gly	240	245	250	1011

GGC TAT AAG AAT TTC TAT GAA AAT TAC CCC CAA TGG TGT GAT CCT CAA 1059
Gly Tyr Lys Asn Phe Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln
255 260 265

5 GGA TAT GTC GAG ATG AAG AAT TTA CGA CAC AAA AAA TTA TGT GAA TCC 1107
Gly Tyr Val Glu Met Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser
270 275 280

10 AAC TTG GAT AAA GTT AGA AAA GAT AAT AAA CTA ACT AGA GCA AAG TCT 1155
Asn Leu Asp Lys Val Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser
285 290 295

15 TAT CAA TTT GGT ATT CAA CAC CGC CGT GGT TCC ACT GGT GGA CTT 1203
Tyr Gln Phe Gly Ile Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu
300 305 310 315

20 TTC GGC AAC TAT AAT TAC AAC GTT ATG AAC TCA TCA GAT CAA CAA TTT 1251
Phe Gly Asn Tyr Asn Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe
320 325 330

25 TGG AGT AGC AGT ACT TCC AAC ACT GCT CAC CAC AGA AGT AGT AGC AGT 1299
Trp Ser Ser Ser Thr Ser Asn Thr Ala His His Arg Ser Ser Ser Ser
335 340 345

30 AGC GGG TTC ATT AAT AAT ATG CAT AGT GGT GCT TCG TCA TAT CAC CAT 1347
Ser Gly Phe Ile Asn Asn Met His Ser Gly Ala Ser Ser Tyr His His
350 355 360

35 CAA AGA TCG ACT CCC AAA GTC AGC AAC TCA CCA ACC AAG CCA CCT CAT 1443
Gln Arg Ser Thr Pro Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His
380 385 390 395

40 CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT 1491
Gln Ser Tyr Leu Ser Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp
400 405 410

45 TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT 1551
CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT 1611
CTGAATTATC AGTCAATACT CAAGATTTTC AACCAACGAC TACGTCCCTT AGGAATT 1668

- 50 (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
55 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 208..513

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AACTTGTAA	CTTATTTGTT	TATATAATTG	ATAGATATCA	ATTACTAATT	TACCCTTGTT	60	
10	TTTTACTTCC	TACTATTCAA	GACTTTATTT	CCTCCTGATA	ATCATTGT	TTGATTATCA	120
	TTTCGTCAA	TTAGTTCTTT	TTTTTCATTT	GTTTCCAGAG	TTTAGGAAGA	CTACCATTT	180
15	ACAATTTCA	ATTCAAATAT	TTTCCCA	ATG ACT AAA	CCA AGA TTT	TTA ACA	231
				Met Thr Lys Pro Arg	Phe Leu Thr		
			1		5		
20	AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC	Arg Tyr Arg Lys Ser Lys Val Gly Ile Ser Asp Met Ile His Tyr	279				
	10	15	20				
25	AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA	Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu	327				
	25	30	35		40		
30	CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA	Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu	375				
	45	50	55				
35	ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA TGG AGA GGG TTA GGA	Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly	423				
	60	65	70				
40	ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG	Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu	471				
	75	80	85				
45	CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA	Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln	513				
	90	95	100				
50	TAAAAAGATT AACTATATT GAATACTATA GAATCGGAAT CGGTTTAAA GTTAACACTG		573				
	GAATTAAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA		633				
55	CCCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTGTATA CACTATTTAT		693				
	AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA		753				
60	AACTGTATAA ATACTCTTGG TACCTCGCAT GTT		786				

(2) INFORMATION FOR SEQ ID NO:3:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 43. . 993

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGAACACAC ACATCCCAAG CCAAGACCAA CACTTATTGC AA ATG GTA GAG TTA		54
Met Val Glu Leu		
1		
TCT GAT TAT CAA CGT CAA GAA AAA GTC GGA GAA GGT ACT TAT GGG GTT		102
Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly Thr Tyr Gly Val		
5	10	15
20		
GTT TAT AAA GCA TTA GAT ACC AAG CAC AAT AAT AGA GTT GTT GCA TTA		150
Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg Val Val Ala Leu		
25	30	35
AAG AAA ATT CGA TTA GAA TCA GAA GAT GAA GGT GTA CCT AGT ACC GCC		198
Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val Pro Ser Thr Ala		
40	45	50
ATT AGA GAA ATC TCG TTA TTA AAA GAA ATG AAA GAT GAT AAT ATC GTT		246
Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp Asp Asn Ile Val		
55	60	65
CGA TTA TAT GAT ATT ATT CAT TCA GAT TCT CAT AAA TTA TAT TTA GTA		294
Arg Leu Tyr Asp Ile Ile His Ser Asp Ser His Lys Leu Tyr Leu Val		
70	75	80
TTT GAA TTT TTG GAT TTA GAT TTA AAG AAA TAT ATG GAA AGT ATT CCT		342
Phe Glu Phe Leu Asp Leu Asp Leu Lys Lys Tyr Met Glu Ser Ile Pro		
85	90	95
100		
CAA GGA GTT GGA CTA GGG GCT AAT ATG ATA AAA AGA TTT ATG AAT CAA		390
Gln Gly Val Gly Leu Gly Ala Asn Met Ile Lys Arg Phe Met Asn Gln		
105	110	115
TTA ATT CGA GGT ATT AAA CAT TGT CAT TCT CAT CGA GTT TTA CAT CGT		438
Leu Ile Arg Gly Ile Lys His Cys His Ser His Arg Val Leu His Arg		
120	125	130
GAT TTA AAA CCA CAA AAT TTA TTG ATT GAT AAA GAA GGG AAT TTA AAA		486
Asp Leu Lys Pro Gln Asn Leu Leu Ile Asp Lys Glu Gly Asn Leu Lys		
135	140	145
TTA GCA GAT TTT GGA TTA GCT CGA GCA TTT GGA GTT CCA TTA AGA GCA		534
Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Ala		
150	155	160
TAT ACT CAT GAA GTC ACT TTA TGG TAT CGA GCT CCC GAA ATC TTG		582
Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu		
165	170	175
180		

TTA GGA GGG AAA CAA TAT TCC ACT GGG GTA GAT ATG TGG TCT GTT GGA Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met Trp Ser Val Gly 185 190 195	630
5 TGT ATA TTT GCT GAA ATG TGT AAT AGG AAA CCA TTA TTT CCT GGT GAT Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu Phe Pro Gly Asp 200 205 210	678
10 TCA GAA ATT GAT GAA ATT TTC CGA ATT TTC CGA ATT TTA GGA ACA CCT Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile Leu Gly Thr Pro 215 220 225	726
15 AAT GAA GAA ATT TGG CCT GAT GTT AAT TAT TTA CCA GAT TTT AAA TCA Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro Asp Phe Lys Ser 230 235 240	774
20 AGT TTC CCT CAA TGG AAA AAG AAA CCT TTG AGT GAA GCA GTT CCA AGT Ser Phe Pro Gln Trp Lys Lys Pro Leu Ser Glu Ala Val Pro Ser 245 250 255 260	822
25 TTG GAT GCT AAT GGA ATT GAT CTT TTG GAT CAA ATG TTG GTG TAT GAT Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met Leu Val Tyr Asp 265 270 275	870
30 CCA AGT AGA AGA ATA AGT GCT AAA CGA GCT TTA ATT CAT CCT TAT TTT Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile His Pro Tyr Phe 280 285 290	918
35 AAT GAT AAT GAT GAT CGT GAT CAT AAC AAT TAT AAT GAA GAT AAT ATT Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn Glu Asp Asn Ile 295 300 305	966
40 GGG ATT GAC AAA CAC CAA AAC ATG CAA TAAATCTTG Gly Ile Asp Lys His Gln Asn Met Gln 310 315	1002

(2) INFORMATION FOR SEQ ID NO:4:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: cDNA
- 50 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 184..1659
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
GCTATTCCCC CCTTTTCCTT TTTTTTATAG AGAAACTTAT TCCAATTACT CATCGAACAA
GATCTTACTA GACTTGTAGA CTCACGACAC GATAAATTAA AATTCAATTAA TCAACCAAACG

60

120

AACCAGCCAA ACCAAAATTA ATTCACATTT ATACTCACTG TTTGTCATTT TCATCTCATA 180
GTA ATG CCA CAA GTC ACT AAA ACT AAT GAA AAT GAG TTT AGA CTT 228
Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu
5 1 5 10 15
ACT AGA TCA AAA GTA CAG CAT CAA GAG TCG ATA AGT ACC ATC AAA AAT 276
Thr Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn
10 20 25 30
ACG ACC ATA TCC AAT TCT CAG CAT AAA CAA CAA ACA CAA CAA CAA ATT 324
Thr Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Ile
15 35 40 45
TCA TCA CCA CCT CAA GTC TCT GTA ACA TCA TCT GAA GGA GTT TCA CAT 372
Ser Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His
20 50 55 60
GTC AAT ACA CGT CAA TAT TTG GGT GAT GTT TCA AAT CAA TAC ATA ACA 420
Val Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr
25 65 70 75
AAT GCT AAA CCA ACA AAT AAA AGA AAA CCA TTG GGT GGA GAC AAT GCC 468
Asn Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala
30 80 85 90 95
CCT CTA CAA AAA CAA CAG CAT AGA CCA TCT AGA CCA ATA CCC ATT GCC 516
Pro Leu Gln Lys Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala
35 100 105 110
AGT GAT AAC AAC AAT AAT GGT AGT ACC AGT AGC AGT AGC AAC AGT AGC 564
Ser Asp Asn Asn Asn Gly Ser Thr Ser Ser Ser Asn Ser Ser
40 115 120 125
AAC AAC AAT AAC AAC GAC GCA AAT AGA CTA GCA TCT TTG GCA GTT CCA 612
Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro
45 130 135 140
TCT CGA TTA CCC CAA AAA CGA CAA GCT ACT GAA TCG TCG ACA AAT TTA 660
Ser Arg Leu Pro Gln Lys Arg Gln Ala Thr Glu Ser Ser Thr Asn Leu
50 145 150 155
GTA GAG AAA TTA AGA GTA CCA CAA CCA GAA GTA GGG GAA AGA AGT CAG 708
Val Glu Lys Leu Arg Val Pro Gln Pro Glu Val Gly Glu Arg Ser Gln
55 160 165 170 175
TCA TAC CAT AAG AAA TCA CGT TTA ATT GAT TAT GAA TGG CAG GAT TTG 756
Ser Tyr His Lys Lys Ser Arg Leu Ile Asp Tyr Glu Trp Gln Asp Leu
60 180 185 190
GAT GAA GAA GAT AAT GAC GAC CAA TTA ATG GTT AGT GAA TAT GTT AAC 804
Asp Glu Glu Asp Asn Asp Gln Leu Met Val Ser Glu Tyr Val Asn
65 195 200 205
GAA ATA TTT TCG TAC TAT TAC GAA TTA GAA ACA CGA ATG TTA CCT GAT 852
Glu Ile Phe Ser Tyr Tyr Tyr Glu Leu Glu Thr Arg Met Leu Pro Asp
70 210 215 220
CCG CAA TAT CTT TTC AAA CAA ACA TTG TTA AAA CCA AGA ATG AGA TCG 900

	Pro Gln Tyr Leu Phe Lys Gln Thr Leu Leu Lys Pro Arg Met Arg Ser		
	225	230	235
5	ATA TTG GTT GAT TGG CTT GTT GAA ATG CAT TTA AAA TTC AAG TTA TTA Ile Leu Val Asp Trp Leu Val Glu Met His Leu Lys Phe Lys Leu Leu		948
	240	245	250
10	CCT GAA TCA CTT TTT TTG GCA GTC AAT GTA ATG GAT AGA TTC ATG TCT Pro Glu Ser Leu Phe Leu Ala Val Asn Val Met Asp Arg Phe Met Ser		996
	260	265	270
15	GTT GAA GTG GTT CAA ATA GAT AAA TTA CAA TTA TTG GCT ACA GCA GCT Val Glu Val Val Gln Ile Asp Lys Leu Gln Leu Leu Ala Thr Ala Ala		1044
	275	280	285
20	TTA TTT ACT GCT GCC AAA AAT GAA GAA GTA TTT TCT CCC CTG GTT AAA Leu Phe Thr Ala Ala Lys Asn Glu Glu Val Phe Ser Pro Ser Val Lys		1092
	290	295	300
25	AAT TAT GCA TAT TTC ACT GAT GGT TCA TAT ACT CCA GAA GAA GTG GTA Asn Tyr Ala Tyr Phe Thr Asp Gly Ser Tyr Thr Pro Glu Glu Val Val		1140
	305	310	315
30	CAA GCA GAA AAA TAC ATG CTT ACC ATT CTT AAC TTT GAT TTG AAT TAC Gln Ala Glu Lys Tyr Met Leu Thr Ile Leu Asn Phe Asp Leu Asn Tyr		1188
	320	325	330
35	CCC AAT CCA ATG AAT TTC TTG AGA AGA ATT TCT AAA GCT GAT GAT TAT Pro Asn Pro Met Asn Phe Leu Arg Arg Ile Ser Lys Ala Asp Asp Tyr		1236
	340	345	350
40	GAT GTC CAA TCA AGA ACG CTA GGA AAA TAT CTT TTG GAA ATC ACT ATA Asp Val Gln Ser Arg Thr Leu Gly Lys Tyr Leu Leu Glu Ile Thr Ile		1284
	355	360	365
45	GTT GAT TAC AAA TTT ATT GGT ATG AGA CCA TCT TTA TGT TGT GCC CTG Val Asp Tyr Lys Phe Ile Gly Met Arg Pro Ser Leu Cys Cys Ala Ser		1332
	370	375	380
50	GCC ATG TAT TTA GCA AGA CTA ATA TTG GGC AAA TTG CCA GTT TGG AAT Ala Met Tyr Leu Ala Arg Leu Ile Leu Gly Lys Leu Pro Val Trp Asn		1380
	385	390	395
55	GGG AAT TTG ATT CAT TAT AGT GGA GGT TAT AGA ATC AGT GAT ATG AGA Gly Asn Leu Ile His Tyr Ser Gly Gly Tyr Arg Ile Ser Asp Met Arg		1428
	400	405	410
60	415		
65	GAA TGT ATC GAA TTA ATG TTT CAA TAT CTT ATT GCT CCT ATA GAA CAT Glu Cys Ile Glu Leu Met Phe Gln Tyr Leu Ile Ala Pro Ile Glu His		1476
	420	425	430
70	GAT GAA TTT TTC AAA AAA TAT GCC ATG AGA AAA TTT ATG AGA GCA AGT Asp Glu Phe Phe Lys Lys Tyr Ala Met Arg Lys Phe Met Arg Ala Ser		1524
	435	440	445
75	ACT CTT TGT CGA AAT TGG GCT AAA AAA TTC CAA GCA TCA GGA AGA GAT Thr Leu Cys Arg Asn Trp Ala Lys Lys Phe Gln Ala Ser Gly Arg Asp		1572
	450	455	460

TTG TTT GAT GAA CGA TTA TCG ACC CAT AGG CTA ACA TTA GAA GAT GAT Leu Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp 465 470 475	1620
5 GAC GAA GAA GAA GAA ATA GTG GTA GCA GAA GCA GAA GAG TAAAGTTTG Asp Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu 480 485 490	1669
10 AGGACTATTG GATCTAGGTT CTTATCTTAA CAATGCATAA ATGAGGAAAT GAAAGAAGAT GAACATGAGT TATGTGCATT ACC	1729
	1752

15 (2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1070 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both	
25 (ii) MOLECULE TYPE: cDNA	
30 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 30..1058	
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
40 ATCAAATCCA TCAGAGAACCCACATCAATC ATG TCT ACT GCA GCA GTT GCA ACG Met Ser Thr Ala Ala Val Ala Thr 1 5	53
45 AAA CCA TCT GTC ACT TCA AAA CCA GCA ACT AAA CAA GTT CTG AAT TAC Lys Pro Ser Val Thr Ser Lys Pro Ala Thr Lys Gln Val Leu Asn Tyr 10 15 20	101
50 ACC AAA GAA AAA AAA GTA GGG GAA GGT ACA TAT GCT GTT GTG TAC TTG Thr Lys Glu Lys Lys Val Gly Glu Gly Thr Tyr Ala Val Val Tyr Leu 25 30 35 40	149
55 GGT AAA CAA ATC TCC ACC AAA CGT CAA ATT GCC ATC AAA GAA ATC AAA Gly Lys Gln Ile Ser Thr Lys Arg Gln Ile Ala Ile Lys Glu Ile Lys 45 50 55	197
60 ACA GGA TTA TTC AAA GAT GGG TTG GAT ATG TCA GCA TTG AGA GAA GTG Thr Gly Leu Phe Lys Asp Gly Leu Asp Met Ser Ala Leu Arg Glu Val 60 65 70	245
65 AAA TAT TTG CAA GAA TTG AAA CAT CCC AAT GTT ATT GAA CTA GTA GAT Lys Tyr Leu Gln Glu Leu Lys His Pro Asn Val Ile Glu Leu Val Asp 75 80 85	293
70 GTA TTT TCA GCA ACA AAT AAT TTA AAT TTG GTA TTA GAA TTT CTA CCT Val Phe Ser Ala Thr Asn Asn Leu Asn Leu Val Leu Glu Phe Leu Pro 90 95 100	341

	TGC GAT TTG GAA GTG TTG ATC AAA GAT AAA TCG ATT GTT TTC AAA TCA Cys Asp Leu Glu Val Leu Ile Lys Asp Lys Ser Ile Val Phe Lys Ser 105 110 115 120	389
5	GCA GAT ATC AAA TCA TGG CTT TTA ATG ACA TTA CGT GGG ATA CAT CAT Ala Asp Ile Lys Ser Trp Leu Leu Met Thr Leu Arg Gly Ile His His 125 130 135	437
10	TGT CAT CGG AAT TTT ATT TTA CAT CGT GAT TTG AAA CCA AAT AAT TTA Cys His Arg Asn Phe Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu 140 145 150	485
15	TTA TTG GCA CCG GAT GGA CAA TTG AAA ATA GCG GAT TTT GGT CTT GCA Leu Leu Ala Pro Asp Gly Gln Leu Lys Ile Ala Asp Phe Gly Leu Ala 155 160 165	533
20	CGA GCT TTG GTA AAT CCT AAT GAA GAT TTA TCA TCT AAT GTT GTC ACT Arg Ala Leu Val Asn Pro Asn Glu Asp Leu Ser Ser Asn Val Val Thr 170 175 180	581
25	AGA TGG TAT AGA GCC CCT GAA TTA TTA TTT GGT GCT CGA CAT TAC ACT Arg Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg His Tyr Thr 185 190 195 200	629
30	GGA GCA GTT GAT ATC TGG TCA ATA GGT ATA ATA TTT GCT GAA TTA ATG Gly Ala Val Asp Ile Trp Ser Ile Gly Ile Ile Phe Ala Glu Leu Met 205 210 215	677
35	CTT CGA ATA CCT TAT TTG CCA GGT AAA GAT GAC GTT GAT CAA TTA GAT Leu Arg Ile Pro Tyr Leu Pro Gly Lys Asp Asp Val Asp Gln Leu Asp 220 225 230	725
40	GTT ACA TTT AGA GCT TAT GGG ACA CCA ACA GAG CAA ATA TGG CCA AAT Val Thr Phe Arg Ala Tyr Gly Thr Pro Thr Glu Gln Ile Trp Pro Asn 235 240 245	773
45	GTT TCC AGT TTG CCA ATG TAT AAT GCA CTT CAT GTG TAT CCA CCT CCT Val Ser Ser Leu Pro Met Tyr Asn Ala Leu His Val Tyr Pro Pro Pro 250 255 260	821
50	TCA AGA CAA GAA TTA CGT AAT AGA TTT AGT GCT GCT ACG GAA AAA GCC Ser Arg Gln Glu Leu Arg Asn Arg Phe Ser Ala Ala Thr Glu Lys Ala 265 270 275 280	869
55	CTT GAT TTG TTG ATA TCG ATG ACC CAA TTG GAT CCA AGT AGA AGA TGT Leu Asp Leu Leu Ile Ser Met Thr Gln Leu Asp Pro Ser Arg Arg Cys 285 290 295	917
60	GAT TCT ACA CTA GCA TTA TTA CAC GAT TAT TTT ACT GAA TCG CCT CGT Asp Ser Thr Leu Ala Leu Leu His Asp Tyr Phe Thr Glu Ser Pro Arg 300 305 310	965
65	CCT ACT GAC CCG AAA AAG TTG CCT AAA AAG TCT TCT CCA GAA AAG AGA Pro Thr Asp Pro Lys Lys Leu Pro Lys Lys Ser Ser Pro Glu Lys Arg 315 320 325	1013
70	GAA AAT GAA GAT GAA CAG AAT GGC TCT AAA AGA AGG CAT GTT Glu Asn Glu Asp Glu Gln Asn Asn Gly Ser Lys Arg Arg His Val	1058

330

335

340

1070

TAGGTTTCTA TA

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..477

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25	TGT TCA GCT ATT GAT ACG AAA AGT TCA GTC TCA GCG ATG GAG CAC AAG Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys 1 5 10 15	48
30	ATT GCT ATA AAG AAA GTA ACA AAG ATT TTC AAC AAA GAC ATC CTT CTA Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu 20 25 30	96
35	ATC AGG GCA ATA CGA GAG CTT AAG TTC ATG ATG TTT TTC AGA GGC CAC Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His 35 40 45	144
40	AAG AAT ATT GCA ACT TTG CTT GAC TTA GAT GTT GTA TAT GTG AAG CCT Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro 50 55 60	192
45	TAT GAA GGC TTG TAT TGT TTT CAA GAG CTA GCC GAT TTA GAT TTA GCT Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala 65 70 75 80	240
50	CGT GTT TTG TAC TCA AAC GTC CAA TTT TCA GAA TTT CAC ATT CAA AGC Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser 85 90 95	288
55	TTT ATG TAC CAA ATT CTT TGC GGA CTC AAG TAC ATC CAT TCT GCT GAT Phe Met Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp 100 105 110	336
60	GTA ATA CAT CGG GAC CTA AAG CCA GGA AAC ATA TTG GTC ACC ACT CAA Val Ile His Arg Asp Leu Lys Pro Gly Asn Ile Leu Val Thr Thr Gln 115 120 125	384
65	GGG ACT TTA AAA ATA TGT GAT TTC GGC TTA GCA CGA GGA ATA AAT CCT Gly Thr Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Ile Asn Pro 130 135 140	432

GTA TAT TTC AGA AAC CGC TCA GCT GTC ATC ACA AAC TAC GTA GCA
Val Tyr Phe Arg Asn Arg Ser Ala Val Ile Thr Asn Tyr Val Ala
145 150 155

477

5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Thr Glu Val Val Ser Lys Ser Ser His Ser Phe Phe Asn Asn Leu
1 5 10 15

20

His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val Ser Ser Thr Thr Pro
20 25 30

25

Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp Asp Ile Pro Thr Asn
35 40 45

30

Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp Thr Phe Ile Gln Ser
50 55 60

35

Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val Thr Thr Thr Ile
65 70 75 80

Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile Tyr Leu Gln Lys Leu
85 90 95

40

Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys Arg Leu His Arg Thr
100 105 110

Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr Asn Ile Glu Tyr Ser
115 120 125

45

His Leu Glu Ser Asp Leu Leu Pro Arg Ile Asp Ala His Gln Leu Ala
130 135 140

Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe Asp Glu Phe Ile Ile
145 150 155 160

50

Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly Gly His Ile Thr Arg
165 170 175

Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln Glu Lys Leu Phe Gln
180 185 190

55

Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser Lys Lys Arg Leu Ile
195 200 205

Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly Pro Met Met Ala Lys
210 215 220

His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr Asp Asn Tyr Pro Leu

225	230	235	240
Leu Thr Tyr Pro Asp Ile Ala Ile Leu Glu Gly Gly Tyr Lys Asn Phe			
245	250	255	
5			
Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln Gly Tyr Val Glu Met			
260	265	270	
Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser Asn Leu Asp Lys Val			
10	275	280	285
Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser Tyr Gln Phe Gly Ile			
290	295	300	
15	Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu Phe Gly Asn Tyr Asn	310	315
305		315	320
Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe Trp Ser Ser Thr			
20	325	330	335
Ser Asn Thr Ala His His Arg Ser Ser Ser Ser Gly Phe Ile Asn			
340	345	350	
25	Asn Met His Ser Gly Ala Ser Ser Tyr His His Arg Ser Gln Ser Phe	355	360
365			
Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg Gln Arg Ser Thr Pro			
370	375	380	
30	Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His Gln Leu Tyr Leu Leu	385	390
395		400	
Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp			
40	405	410	
35			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:			
40	(A) LENGTH: 102 amino acids		
	(B) TYPE: amino acid		
	(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: protein			
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:		
Met Thr Lys Pro Arg Phe Leu Thr Arg Tyr Arg Lys Ser Lys Ser Val			
	1	5	10
50	15		
Gly Ile Ser Asp Met Ile His Tyr Ser Pro Arg Tyr Ser Asp Asp Ser			
	20	25	30
55	Tyr Glu Tyr Arg His Val Met Leu Pro Lys Asn Met Leu Lys Ala Ile	35	40
	45		
Pro His Asp Tyr Phe Asn Gln Glu Thr Gly Thr Leu Arg Ile Leu Thr			
	50	55	60

Glu Glu Glu Trp Arg Gly Leu Gly Ile Thr Gln Ser Leu Gly Trp Ala
65 70 75 80

His Tyr Glu Thr His Ala Pro Glu Pro His Ile Leu Leu Phe Lys Arg
5 85 90 95

Pro Leu Asn Pro Gly Gln
100

10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Val Glu Leu Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly
1 5 10 15

25

Thr Tyr Gly Val Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg
20 25 30

30

Val Val Ala Leu Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val
35 40 45

Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp
50 55 60

35

Asp Asn Ile Val Arg Leu Tyr Asp Ile Ile His Ser Asp Ser His Lys
65 70 75 80

45

Leu Tyr Leu Val Phe Glu Phe Leu Asp Leu Asp Leu Lys Lys Tyr Met
85 90 95

40

Glu Ser Ile Pro Gln Gly Val Gly Leu Gly Ala Asn Met Ile Lys Arg
100 105 110

Phe Met Asn Gln Leu Ile Arg Gly Ile Lys His Cys His Ser His Arg
115 120 125

Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Ile Asp Lys Glu
130 135 140

50

Gly Asn Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val
145 150 155 160

55

Pro Leu Arg Ala Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala
165 170 175

Pro Glu Ile Leu Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met
180 185 190

Trp Ser Val Gly Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu
195 200 205

Phe Pro Gly Asp Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile
210 215 220

5 Leu Gly Thr Pro Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro
225 230 235 240

Asp Phe Lys Ser Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu
245 250 255

10 Ala Val Pro Ser Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met
260 265 270

Leu Val Tyr Asp Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile
15 275 280 285

His Pro Tyr Phe Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn
290 295 300

20 Glu Asp Asn Ile Gly Ile Asp Lys His Gln Asn Met Gln
305 310 315

(2) INFORMATION FOR SEQ ID NO:10:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35 Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu Thr
1 5 10 15

Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn Thr
20 25 30

40 Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Ile Ser
35 40 45

45 Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His Val
50 55 60

Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr Asn
65 70 75 80

50 Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala Pro
85 90 95

Leu Gln Lys Gln Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala Ser
100 105 110

55 Asp Asn Asn Asn Asn Gly Ser Thr Ser Ser Ser Asn Ser Ser Asn
115 120 125

Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro Ser

	130	135	140
	Arg Leu Pro Gln Lys Arg Gln Ala Thr Glu Ser Ser Thr Asn Leu Val		
5	145	150	155
	Glu Lys Leu Arg Val Pro Gln Pro Glu Val Gly Glu Arg Ser Gln Ser		
	165	170	175
10	Tyr His Lys Lys Ser Arg Leu Ile Asp Tyr Glu Trp Gln Asp Leu Asp		
	180	185	190
	Glu Glu Asp Asn Asp Asp Gln Leu Met Val Ser Glu Tyr Val Asn Glu		
	195	200	205
15	Ile Phe Ser Tyr Tyr Glu Leu Glu Thr Arg Met Leu Pro Asp Pro		
	210	215	220
	Gln Tyr Leu Phe Lys Gln Thr Leu Leu Lys Pro Arg Met Arg Ser Ile		
20	225	230	235
	Leu Val Asp Trp Leu Val Glu Met His Leu Lys Phe Lys Leu Leu Pro		
	245	250	255
25	Glu Ser Leu Phe Leu Ala Val Asn Val Met Asp Arg Phe Met Ser Val		
	260	265	270
	Glu Val Val Gln Ile Asp Lys Leu Gln Leu Leu Ala Thr Ala Ala Leu		
	275	280	285
30	Phe Thr Ala Ala Lys Asn Glu Glu Val Phe Ser Pro Leu Val Lys Asn		
	290	295	300
	Tyr Ala Tyr Phe Thr Asp Gly Ser Tyr Thr Pro Glu Glu Val Val Gln		
35	305	310	315
	Ala Glu Lys Tyr Met Leu Thr Ile Leu Asn Phe Asp Leu Asn Tyr Pro		
	325	330	335
40	Asn Pro Met Asn Phe Leu Arg Arg Ile Ser Lys Ala Asp Asp Tyr Asp		
	340	345	350
	Val Gln Ser Arg Thr Leu Gly Lys Tyr Leu Leu Glu Ile Thr Ile Val		
	355	360	365
45	Asp Tyr Lys Phe Ile Gly Met Arg Pro Ser Leu Cys Cys Ala Leu Ala		
	370	375	380
	Met Tyr Leu Ala Arg Leu Ile Leu Gly Lys Leu Pro Val Trp Asn Gly		
50	385	390	395
	Asn Leu Ile His Tyr Ser Gly Gly Tyr Arg Ile Ser Asp Met Arg Glu		
	405	410	415
55	Cys Ile Glu Leu Met Phe Gln Tyr Leu Ile Ala Pro Ile Glu His Asp		
	420	425	430
	Glu Phe Phe Lys Lys Tyr Ala Met Arg Lys Phe Met Arg Ala Ser Thr		
	435	440	445

Leu Cys Arg Asn Trp Ala Lys Lys Phe Gln Ala Ser Gly Arg Asp Leu
450 455 460

5 Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp Asp
465 470 475 480

Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu
485 490

10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 343 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Thr Ala Ala Val Ala Thr Lys Pro Ser Val Thr Ser Lys Pro
1 5 10 15

25 Ala Thr Lys Gln Val Leu Asn Tyr Thr Lys Glu Lys Lys Val Gly Glu
20 25 30

30 Gly Thr Tyr Ala Val Val Tyr Leu Gly Lys Gln Ile Ser Thr Lys Arg
35 40 45

Gln Ile Ala Ile Lys Glu Ile Lys Thr Gly Leu Phe Lys Asp Gly Leu
50 55 60

35 Asp Met Ser Ala Leu Arg Glu Val Lys Tyr Leu Gln Glu Leu Lys His
65 70 75 80

40 Pro Asn Val Ile Glu Leu Val Asp Val Phe Ser Ala Thr Asn Asn Leu
85 90 95

45 Asn Leu Val Leu Glu Phe Leu Pro Cys Asp Leu Glu Val Leu Ile Lys
100 105 110

Asp Lys Ser Ile Val Phe Lys Ser Ala Asp Ile Lys Ser Trp Leu Leu
115 120 125

50 Met Thr Leu Arg Gly Ile His His Cys His Arg Asn Phe Ile Leu His
130 135 140

55 Arg Asp Leu Lys Pro Asn Asn Leu Leu Ala Pro Asp Gly Gln Leu
145 150 155 160

Lys Ile Ala Asp Phe Gly Leu Ala Arg Ala Leu Val Asn Pro Asn Glu
165 170 175

Asp Leu Ser Ser Asn Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu
180 185 190

Leu Phe Gly Ala Arg His Tyr Thr Gly Ala Val Asp Ile Trp Ser Ile

195 200 205
Gly Ile Ile Phe Ala Glu Leu Met Leu Arg Ile Pro Tyr Leu Pro Gly
210 215 220
5 Lys Asp Asp Val Asp Gln Leu Asp Val Thr Phe Arg Ala Tyr Gly Thr
225 230 235 240
Pro Thr Glu Gln Ile Trp Pro Asn Val Ser Ser Leu Pro Met Tyr Asn
10 245 250 255
Ala Leu His Val Tyr Pro Pro Ser Arg Gln Glu Leu Arg Asn Arg
260 265 270
15 Phe Ser Ala Ala Thr Glu Lys Ala Leu Asp Leu Leu Ile Ser Met Thr
275 280 285
Gln Leu Asp Pro Ser Arg Arg Cys Asp Ser Thr Leu Ala Leu Leu His
290 295 300
20 Asp Tyr Phe Thr Glu Ser Pro Arg Pro Thr Asp Pro Lys Lys Leu Pro
305 310 315 320
Lys Lys Ser Ser Pro Glu Lys Arg Glu Asn Glu Asp Glu Gln Asn Asn
25 325 330 335
Gly Ser Lys Arg Arg His Val
340
30 (2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
35 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
40 Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys
1 5 10 15
Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu
45 20 25 30
Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His
35 40 45
50 Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro
50 55 60
Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala
65 70 75 80
55 Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser
85 90 95

Phe Met Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp
100 105 110

5 Val Ile His Arg Asp Leu Lys Pro Gly Asn Ile Leu Val Thr Thr Gln
115 120 125

Gly Thr Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Ile Asn Pro
130 135 140

10 Val Tyr Phe Arg Asn Arg Ser Ala Val Ile Thr Asn Tyr Val Ala
145 150 155

15 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1019 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1017

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG AAG TTG TCA GAT TAT TAT ATA GAC AAG GAA TTA ATT TAC AAT AGT	48
Met Lys Leu Ser Asp Tyr Tyr Ile Asp Lys Glu Leu Ile Tyr Asn Ser	
1 5 10 15	
35 GCC ATT TCT GAT ATA TAT ACG GCT ATT GAT AAG TTT AAT AAC TTA CCA	96
Ala Ile Ser Asp Ile Tyr Thr Ala Ile Asp Lys Phe Asn Asn Leu Pro	
20 25 30	
40 GTA TGT CTT AAA ATA GTT GAT GAA GAT TTC AGT CTT CCA CCA CAT TCA	144
Val Cys Leu Lys Ile Val Asp Glu Asp Phe Ser Leu Pro Pro His Ser	
35 40 45	
45 ATC CAT CGA GAA ATT TTT ATA CTT AAA ACT TTG AAA CCA CAT CCA AAC	192
Ile His Arg Glu Ile Phe Ile Leu Lys Thr Leu Lys Pro His Pro Asn	
50 55 60	
50 ATA ATT GAA TAT TTT AAT GAT CTT AAA ATT TAT GAT GAT GTT ATA TTA	240
Ile Ile Glu Tyr Phe Asn Asp Leu Lys Ile Tyr Asp Asp Val Ile Leu	
65 70 75 80	
55 GTC ACC AAA TTG TAT CGT TAT GAT TTG AGT CAA TTG ATT GAA ATT ACA	288
Val Thr Lys Leu Tyr Arg Tyr Asp Leu Ser Gln Leu Ile Glu Ile Thr	
85 90 95	
60 AAA TAT TGT AAA CGA ACA ACA CGA TTT ATT TAT GGT ATT AAT GGT AAT	336
Lys Tyr Cys Lys Arg Thr Arg Phe Ile Tyr Gly Ile Asn Gly Asn	
100 105 110	
65 CTT GTT AGT AAT CAA TAT ACA CTT GCT AAT GAA ATT GAA GAA AAA GAT	384
Leu Val Ser Asn Gln Tyr Thr Leu Ala Asn Glu Ile Glu Glu Lys Asp	
115 120 125	
65 ATC AAA TTA TGG TTA AAA TCA ATG AGT TCA GGA CTT GAA TTT ATT CAT	432
Ile Lys Leu Trp Leu Lys Ser Met Ser Ser Gly Leu Glu Phe Ile His	

	130	135	140		
	TCA CAA GGG ATA ATT CAT CGT GAT ATA AAA CCC AGT AAT ATT TTC TTT			480	
5	Ser Gln Gly Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Phe Phe				
	145	150	155	160	
	GCC CGG GAT GAT ATA ACA CAA CCG ATT ATT GGA GAT TTT GAT ATT TGT			528	
	Ala Arg Asp Asp Ile Thr Gln Pro Ile Ile Gly Asp Phe Asp Ile Cys				
10	165	170	175		
	TAT GAT TTA AAA CTG CCA CCT AAA GAT GAA CCC CCT ATG GCG AAA TAT			576	
	Tyr Asp Leu Lys Leu Pro Pro Lys Asp Glu Pro Pro Met Ala Lys Tyr				
	180	185	190		
15	ATT GAT GTA TCT ACA GGT ATT TAT AAA GCA CCA GAA TTG ATT CTT GGT			624	
	Ile Asp Val Ser Thr Gly Ile Tyr Lys Ala Pro Glu Leu Ile Leu Gly				
	195	200	205		
20	ATA ACT AAT TAT GAA TAT GAA ATT GAT ATT TGG TCA TTG GGT ATA ATT			672	
	Ile Thr Asn Tyr Glu Tyr Ile Asp Ile Trp Ser Leu Gly Ile Ile				
	210	215	220		
25	TTG ACT GGT TTA TAT TCA GAA AAT TTT CAA AGT GTT TTA GTC AAA GAT			720	
	Leu Thr Gly Leu Tyr Ser Glu Asn Phe Gln Ser Val Leu Val Lys Asp				
	225	230	235	240	
	GAT AAA GAA TTG ACT AAT GAT TCT CAT GTT AGT GAT TTA TAT TTA TTA			768	
	Asp Lys Glu Leu Thr Asn Asp Ser His Val Ser Asp Leu Tyr Leu Leu				
	245	250	255		
30	AAT CAA ATA TTT GAA AAT TTC GGT ACA CCC AAT TTA ACT GAT TTT GAA			816	
	Asn Gln Ile Phe Glu Asn Phe Gly Thr Pro Asn Leu Thr Asp Phe Glu				
	260	265	270		
35	GAT GAA TTA TTT TGT GAT GAA TAT AAT GAA AAC TTG CAT TTT AAA			864	
	Asp Glu Leu Phe Cys Asp Glu Tyr Asn Asn Glu Asn Leu His Phe Lys				
	275	280	285		
40	AAA TTC AAT TTA CAA AAA TAT CCT AGA AAA GAT TGG GAT ATT ATT TTA			912	
	Lys Phe Asn Leu Gln Lys Tyr Pro Arg Lys Asp Trp Asp Ile Ile Leu				
	290	295	300		
45	CCT CGA TGC AAT GAT GAT TTA ATG AAA GAA ATT TTT ACC AAG ATG ATT			960	
	Pro Arg Cys Asn Asp Asp Leu Met Lys Glu Ile Phe Thr Lys Met Ile				
	305	310	315	320	
	AGA TAT GAT CGA AGT AAA AGA ATA ACT TCT AAA GAA ATC TTA CAA TTA			1008	
	Arg Tyr Asp Arg Ser Lys Arg Ile Thr Ser Lys Glu Ile Leu Gln Leu				
	325	330	335		
50	ATG TTG GAT TG			1019	
	Met Leu Asp				
55	(2) INFORMATION FOR SEQ ID NO:14:				

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Leu Ser Asp Tyr Tyr Ile Asp Lys Glu Leu Ile Tyr Asn Ser

1 5 10 15
Ala Ile Ser Asp Ile Tyr Thr Ala Ile Asp Lys Phe Asn Asn Leu Pro
20 25 30
5 Val Cys Leu Lys Ile Val Asp Glu Asp Phe Ser Leu Pro Pro His Ser
35 40 45
Ile His Arg Glu Ile Phe Ile Leu Lys Thr Leu Lys Pro His Pro Asn
10 50 55 60
Ile Ile Glu Tyr Phe Asn Asp Leu Lys Ile Tyr Asp Asp Val Ile Leu
65 70 75 80
15 Val Thr Lys Leu Tyr Arg Tyr Asp Leu Ser Gln Leu Ile Glu Ile Thr
85 90 95
Lys Tyr Cys Lys Arg Thr Thr Arg Phe Ile Tyr Gly Ile Asn Gly Asn
20 100 105 110
Leu Val Ser Asn Gln Tyr Thr Leu Ala Asn Glu Ile Glu Glu Lys Asp
115 120 125
25 Ile Lys Leu Trp Leu Lys Ser Met Ser Ser Gly Leu Glu Phe Ile His
130 135 140
Ser Gln Gly Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Phe Phe
145 150 155 160
30 Ala Arg Asp Asp Ile Thr Gln Pro Ile Ile Gly Asp Phe Asp Ile Cys
165 170 175
Tyr Asp Leu Lys Leu Pro Pro Lys Asp Glu Pro Pro Met Ala Lys Tyr
35 180 185 190
Ile Asp Val Ser Thr Gly Ile Tyr Lys Ala Pro Glu Leu Ile Leu Gly
195 200 205
40 Ile Thr Asn Tyr Glu Tyr Glu Ile Asp Ile Trp Ser Leu Gly Ile Ile
210 215 220
Leu Thr Gly Leu Tyr Ser Glu Asn Phe Gln Ser Val Leu Val Lys Asp
225 230 235 240
45 Asp Lys Glu Leu Thr Asn Asp Ser His Val Ser Asp Leu Tyr Leu Leu
245 250 255
Asn Gln Ile Phe Glu Asn Phe Gly Thr Pro Asn Leu Thr Asp Phe Glu
50 260 265 270
Asp Glu Leu Phe Cys Asp Glu Tyr Asn Asn Glu Asn Leu His Phe Lys
275 280 285
55 Lys Phe Asn Leu Gln Lys Tyr Pro Arg Lys Asp Trp Asp Ile Ile Leu
290 295 300
Pro Arg Cys Asn Asp Asp Leu Met Lys Glu Ile Phe Thr Lys Met Ile
305 310 315 320
60 Arg Tyr Asp Arg Ser Lys Arg Ile Thr Ser Lys Glu Ile Leu Gln Leu
325 330 335
Met Leu Asp